



SEQUENCE LISTING

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<110> Maliszewski, Charles R.
Gayle III, Richard B.
Price, Virginia L.
Gimpel, Steven D.

<120> INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT

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<150> US 60/104,585

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<160> 37

<170> PatentIn version 3.1

<210> 1

<211> 1599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1596)

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ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser

1

5

10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156

Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile

15

20

25

30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204

Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn

35

40

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gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu

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55

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tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 95 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 444
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125

tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 492
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140

gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 540
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 588
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 160 165 170

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 636
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 175 180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 684
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 732
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 780
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 828
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 240 245 250

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 876
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 255 260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 924
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 972
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 1020
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
305 310 315

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1068
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
320 325 330

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1116
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
335 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1164
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
400 405 410

A2 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
415 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
465 470 475

ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
480 485 490

ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
495 500 505 510

tag 1599

<210> 2
<211> 510
<212> PRT
<213> Homo sapiens

<400> 2

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Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
20 25 30

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
 485 490 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
 500 505 510

<210> 3
 <211> 476
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 3

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 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35 40 45

A2 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 4

<211> 476

<212> PRT

<213> Artificial Sequence

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<223> Fusion construct of human CD39

<220>

<221> MISC_FEATURE

<222> (39)..(39)

<223> Any amino acid, preferably Cys or Ser

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 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 5
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct of human CD39

<220>
<221> CDS
<222> (1)..(1362)
<223>

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Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240
 Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
 65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288
 Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
 85 90 95

tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336
 Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
 100 105 110

cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384
 Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
 115 120 125

gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432
 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
 130 135 140

agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480
 Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
 145 150 155 160

aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528
 Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
 165 170 175

gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576
 Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
 180 185 190

ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc 624
 Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
 195 200 205

gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac 672
 Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
 210 215 220

aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc 720
 Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
 225 230 235 240

tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc 768
 Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
 245 250 255

agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt 816
 Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
 260 265 270

gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca 864
 Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
 275 280 285

ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat 912
 Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
 290 295 300

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag 960
 Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
 305 310 315 320

tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg 1008
 Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
 325 330 335

gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca 1056
 Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
 340 345 350

gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt 1104
 Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
 355 360 365

gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag 1152
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
 370 375 380

aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc 1200
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
 385 390 395 400

ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat 1248
 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
 405 410 415

ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac 1296
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
 420 425 430

atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca 1344
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
 435 440 445

cct ctc tcc cac tcc acc taa 1365
 Pro Leu Ser His Ser Thr
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<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

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<223> Fusion construct of human CD39

<400> 6

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 1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
 20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
 35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
165 170 175

Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
180 185 190

Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
195 200 205

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
210 215 220

Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
225 230 235 240

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
245 250 255

Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
260 265 270

Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
275 280 285

Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
290 295 300

Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
305 310 315 320

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
325 330 335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
435 440 445

Pro Leu Ser His Ser Thr
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<210> 7
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (1)..(1434)
<223>

<400> 7

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 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys
 20 25 30

aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 288
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 336
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 384
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125

tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 432
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140

gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 480
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155 160

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 528
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 165 170 175

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 576
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 624
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 672
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 720
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 768
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 816
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 864
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 912
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 960
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1008
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 325 330 335

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1056
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1104
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
 355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1152
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
 370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1200
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
 385 390 395 400

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1248
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
 405 410 415

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1296
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1344
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
 435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1392
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
 450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa 1437
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 8
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 8

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80

His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95

Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110

Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155 160

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 165 170 175

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 180 185 190

Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300

Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
 340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
 355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
 370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
 385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
 405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr
 420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
 435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
 450 455 460

Pro Ala Glu Gln Pro^oLeu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 9
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser
 20

<210> 10
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 11
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 11

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
 35 40

<210> 12
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 12

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
 20 25

<210> 13
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 13

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
 20 25 30

<210> 14
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 14
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctcccac gagcccc 87

<210> 15
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 15
 gatcggggct cgtgggagag aggtgtggac aatgggttgct cagctgggat catgttggtc 60

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<210> 16
<211> 740
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (42) .. (737)
<223>
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<400>	16															56
cggtaccgct	agcgtcgaca	ggcctaggat	atcgatacgt	a	gag	ccc	aga	tct	tgt							
					Glu	Pro	Arg	Ser	Cys							
					1				5							
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	gcc	gag	ggc	104
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	
			10						15					20		
gcg	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	152
Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			25					30					35			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	200
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		40					45					50				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	248
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	55					60					65					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	296
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
70					75					80					85	
cgg	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	344
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				90					95					100		
aag	gac	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atg	392
Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Met	
			105					110					115			
cag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	440
Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		120					125					130				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	488
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	135					140					145					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agg	cac	atc	gcc	gtg	gag	536
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	Ala	Val	Glu	
150					155				160						165	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	584
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	

	170	175	180	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg				632
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val				
	185	190	195	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg				680
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met				
	200	205	210	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct				728
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser				
	215	220	225	
ccg ggt aaa tga				740
Pro Gly Lys				
230				
<210> 17				
<211> 232				
<212> PRT				
<213> Homo sapiens				
<400> 17				
Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala				
1 5 10 15				
Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro				
20 25 30				
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val				
35 40 45				
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val				
50 55 60				
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln				
65 70 75 80				
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln				
85 90 95				
Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala				
100 105 110				
Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro				
115 120 125				
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr				
130 135 140				

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 18
ctttccatcc tgagcaac

18

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 19
aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20
<211> 24
<212> PRT
<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser

20

<210> 21
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 21
 ctagttcttg agactacaaa gatgacgatg acaaaaccca gaacaa 46

<210> 22
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 22
 agctttgttc tgggttttgt catcgatc tttgtagtct ccagaa 46

<210> 23
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 23
 ccggttgac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctcccac tccacctaa 89

<210> 24
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 24
 ggccttaggt ggagtgggag agaggtgtgg acaatggttg ctcagctggg atcatgttgg 60
 tcaggttcag catgtagccc aaagtccag 89

<210> 25
 <211> 1464
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<220>

<221> CDS

<222> (1)..(1461)

<223>

<400> 25

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta	48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu	
1 5 10 15	

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa	144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Lys	
35 40 45	

acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg	192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu	
50 55 60	

gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca	240
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala	
65 70 75 80	

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	
85 90 95	

gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata	336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	
100 105 110	

ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca	384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	
115 120 125	

agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc	432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	
130 135 140	

atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg	480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	
145 150 155 160	

gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt	528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	
165 170 175	

gcc agg atc att act ggc caa gag gaa ggt gcc tat gcc tgg att act	576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	
180 185 190	

atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc	624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	
195 200 205	

ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac 672
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
 210 215 220

ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act 720
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
 225 230 235 240

atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac 768
 Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
 245 250 255

tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca 816
 Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
 260 265 270

ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att 864
 Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
 275 280 285

ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta 912
 Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
 290 295 300

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt 960
 Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
 305 310 315 320

cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc 1008
 Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
 325 330 335

cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc 1056
 His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
 340 345 350

cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt 1104
 Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
 355 360 365

ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca 1152
 Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
 370 375 380

tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc 1200
 Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
 385 390 395 400

tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag 1248
 Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
 405 410 415

gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc 1296
 Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
 420 425 430

ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc 1344
 Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
 435 440 445

cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc 1392

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
 450 455 460

tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc 1440
 Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
 465 470 475 480

aca cct ctc tcc cac tcc acc taa 1464
 Thr Pro Leu Ser His Ser Thr
 485

<210> 26
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct of human CD39

<400> 26

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
 85 90 95

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
 100 105 110

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
 115 120 125

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
 130 135 140

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
 145 150 155 160

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
 165 170 175

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
 180 185 190

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
 195 200 205

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
 210 215 220

Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
 225 230 235 240

Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
 245 250 255

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
 260 265 270

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
 275 280 285

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
 290 295 300

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
 305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
 325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
 340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
 355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
 370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
 385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
 405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
 420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
 435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
 450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
 465 470 475 480

Thr Pro Leu Ser His Ser Thr
 485

<210> 27
 <211> 464
 <212> PRT
 <213> Artificial Sequence

CA <220>
 <223> Fusion construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
 20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
 35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
 50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser
 65 70 75 80

Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys
 85 90 95

Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr
 100 105 110

Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu
115 120 125

Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu
130 135 140

Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln
145 150 155 160

Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys
165 170 175

Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn
180 185 190

Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln
195 200 205

Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala
210 215 220

Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser
225 230 235 240

Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys
245 250 255

Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His
260 265 270

Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro
275 280 285

Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile
290 295 300

Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu
305 310 315 320

Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile
325 330 335

Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr
340 345 350

Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu
355 360 365

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
370 375 380

Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
385 390 395 400

Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His
405 410 415

Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 28
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
130 135 140

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
145 150 155 160

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
165 170 175

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg
180 185 190

Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly
195 200 205

Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln
210 215 220

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
225 230 235 240

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
245 250 255

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
260 265 270

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
275 280 285

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
290 295 300

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
305 310 315 320

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
325 330 335

Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
 340 345 350

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
 355 360 365

Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
 370 375 380

Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
 385 390 395 400

Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
 405 410 415

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
 420 425 430

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
 435 440 445

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
 20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
 35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
 50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
260 265 270

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
275 280 285

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
290 295 300

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
305 310 315 320

Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
325 330 335

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
340 345 350

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
355 360 365

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
370 375 380

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
385 390 395 400

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
405 410 415

Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
420 425 430

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
145 150 155 160

a2 Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys
275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly

20

25

30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
 50 55

<210> 32
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker sequence

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
 1 5 10

<210> 33
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker sequence

<400> 33

Gly Ala Gly Gly Ala Gly Ser Gly Gly Gly Gly Gly Ser
 1 5 10

<210> 34
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker sequence

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 35
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker sequence

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro
1 5

<210> 36

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

al

Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser
20 25

<210> 37

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 37

Thr Ser Ser Gly
1
